gb_gss14:*
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gb_gss17:* gb_gss13:* em_gssl3:* gb_gss19:* gb_gss18:*

SOURCE

ORGANISM

Bos taurus.

AW657531.1 GI:7423429

KEYWORDS VERSION

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	_	-	42	41	c 40	39	38	c 37	ω	c - 35			32	31	30	29		c 27	26	25	24	23		c 21		c 19	14	17	15		13		c 11		o c	0		c)	C	• u		, -		Result No.
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RESULT AW657531

LOCUS AW657531 549 bp mRNA EST (
DEFINITION 110922 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AW657531

ALIGNMENTS

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FEATURES
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Best Local 9
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6843 caatactgggftaaccccctgtgttttccacctcagtcttccaaccaatccaaagatttctg 6902
                                                                                    6783 ttatgagcaggcctcagaaaatcagtatttagtacctggttataacaggtggtggtgggcatg 6842
                                                                                                                                              6663 tagaaatcaatgtacatgggggtcccgaaataagcttaccctcactgaagtttccgggaa 6722
                                                                                                                                                                                                                                                                                                                                                          6603 agggcctccttattatgaggggatggctaaagaaagaaaattcaatgtgaccaaagagca 6662
                                                                                                                                                                                                                                                                                                                                                                                                                          6543 ccaagccatcaactccaccgaccctgatgccacttcttcttgttggctttgtctatcctc 6602
                                                                                                                                                                                                                                   182 TAGAAATCAATGTACATGGGGGTCCCGAAATAAGCTCACCCTCACTGAAGTTTCCGGGAA 241
                                                                                                                                                                                                                                                                                                                    122 AGGGCCTCCTTATTATGAGGGAATGGCTAGAGAAGGGAAATTCAATGTGACCAAAGAGCA 181
                                                              302 TTATGAGCAGGCCTTAGAAAATCAGTATTTAGTACCTGGTTATAACTGATGGTGGGCATG
                                                                                                                                                                                                                                                                                                                                                                                                      62 CCAAGCCATCAACTCCACCGACCCCGATGCCAGTTCTTCTTGTTTGGCTTTGTCTATCCTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle Unpublished (2000) on Oct 30, 1998 this sequence version replaced gi:3815947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD: GTTTTCCCAGTCACGACG
Plate: 94 row: E column: 12
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Fax: 402 762 4390
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144 c 121 g 139 t
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/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
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/lab_host="DH10B"
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2725 ctcgagaaggaatttggccgcatgttcaaagattaatccaacagggcatcctagttcctg 2784
                                                                                                         2665 ttcaactgaaggccagtgctacaccagtatcagtcagacagtaccccttgagtagagagg 2724
                                                                                                                                                                                            2605 cccaagcctgggcagaaaccgcagggatgggtttggcaaagcaagttcccccacaggtta 2664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bource
                                                                61 TACCTCTAAAGGCAACCTCCACCCCTGTGTCCATCAAACAGTACCCCCATGTCACACGAAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 TGTCATGGTCCAGCTCGTCCCCTGGGTACACTACCATCCTGAGGAAGTAGTCATCGATGA 481
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                                                                                                                                                     CCCAGGCCTGGGCAGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCGCCTCTGATTA 60
                                                                                                                                                                                                                                                       447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Can Research Center (DKP2); Email s. Wiemann@dkfz- heidelberg.de; sequenced by LMU (Ludwig Maximilians University,
                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone (DKFZp762K0910) is available at the RZPD in Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please contact the RZPD: Ressourcenzentrum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No s1 sequence available.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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1 (bases 1 to 632)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H., Bauersachs, S., Mewes, W., Weil, B. and Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
/lab_host="DH10B"
/note="Vector: pSportl; Site_1: NotI; Site_2: SalI"
/195 c 143 g 132 t
                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="DKFED762K0910"
/clone_lib="762 (synonym: hmel2)"
/tlssue_type="melanoma (MeWo cell line)"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                       4.18;
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                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3145 tcaggatccaacaccctcaggtgaccctcctccagtacgtggatgacctgcttctggcgg 3204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3025 togaatggagagatccaggtacggggaagaaccggggcagctcacctggacccgactgcccc 3084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2845 gaccagtacaggacttgagagaggtcaataaaagggtgcaggacatacacccaacggtcc 2904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2785 tocaatccccttggaatactcccctgctaccggttaggaagcctgggaccaatgattatc 2844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 TTGAGTGGAGAGATCCAGAAATGGGAATCTCTGGACAATTGACCTGGACCAGACTCCCAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GCCAGTCCCCTGGAACACACCCCTGCTGCTGCCCGTTAAGAAACCAGGGACTAATGATTACA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CCAGACTGGGGATCAAGCCCCCACATACAGAGACTGTTGGACCAGGGAATATTGGTACCTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGTTTCAAAAACAGTCCCACCCTGTTTGATGAGGCATTGCACAGAGACCTAGCAGACT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTACTTCCGAACTAGACTGCCAACAAGGTAC 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAATCCTTACAACCTCTTAAGTGGACTCCCTCCGTCCCACCAGTGGTACACTGTGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aagggttcaagaactccccgaccatctttgacgaagccctacacagggacctggccaact 3144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTAAAAGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTTGCCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acttaaaagatgccttcttctgcctgagattacaccccactagccaaccactttttgcct 3024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cyaacccttataacctcttgagcgccctcccgcctgaacggaactggtacacagtattgg 2964
                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
Plate: 25 row: D column: 18
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
Single pass sequencing. Bases call
v0.980904.e. Vector identified by
and minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                      On Jul 9, 1999 this sequence version replaced g1:5866807. Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                             FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                      PCR PRimers
                                                                                                                                                                                                                                                                                                                                                        Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST discovery in swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A. and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fahrenkrug, S.C.,
Stone, R.T., Heato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 345)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43799 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW358862.1 GI:6863512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW358862
/db_xref="taxon:9823"
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/tissue_type="pooled"
                                                                       /organism="Sus scrofa"
                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (2000)
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                                                                                                                                                                                                                                                                                             called and trimmed with phred
                                                                                                                                                                                                                                                                              cross_match with the
                                                                                                                                                                                                                                                                         -minscore 20
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